



SEQUENCE LISTING

<110> Lechler, Robert
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION

<130> 02292/000H795-US0

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/GB99/01350

<151> 1999-04-30

<150> GB-9809280.2

<151> 1998-04-30

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

<400> 1

Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
1 5 10 15
Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30
Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60
Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80
Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175
Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 2
<211> 672
<212> DNA
<213> Sus scrofa

<400> 2
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gccaacctg cagtagtgct ggccaacagc cggggtgttg ccagctttgt gtgtgagtat 180
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atgactgaag tctgtgccgc gacatatact gtggaggatg agttgacctt ccttgatgac 300
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gtgggtatgg gcaacgggac ccagatttat gtcattgatc cagaaccatg cccagattct 480
gatttcctgc tctggatcct ggcagcagtt agttcagggt tgttttttta cagcttcctc 540
atcacagctg tttctttgag caaaatgcta aagaaaagaa gtcctcttac tacaggggtc 600
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cccatcaatt ga 672

<210> 3
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pCTLA4-Ig construct (Figure 4)

<400> 3
Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30
Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60
Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80
Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
2

145 150 155 160
 Asp Gly Gly Ser Gly Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr
 165 170 175
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 180 185 190
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 195 200 205
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 210 215 220
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 225 230 235 240
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 245 250 255
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 260 265 270
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 275 280 285
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 290 295 300
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 305 310 315 320
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 325 330 335
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 340 345 350
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 355 360 365
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 370 375 380
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395 400

<210> 4
 <211> 722
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 4
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 ctccagggaa ggggctggag tgggtctcag ctattcgtgg tagtgggtgg agcacatact 180
 acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag aacacgctgt 240
 atctgcaaat gaacagcctg agagccgagg acacggccgt gtattactgt gcaagagctg 300
 gtcgtatttt gtttgactat tggggccaag gtaccctggc caccgtctcg agtgggtggag 360
 gcggttcagg cggaggtggc tctggcggtg gtgcacttca gtctgtgctg actcagccac 420

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cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctgga agcagctcca 480
acatcggaag taattatgta tactgggtacc agcagctccc aggaacggcc cccaaactcc 540
tcatttatag gaataatcag cggccctcag gggtccttga ccgattctct ggctccaagt 600
ctggcacctc agcctcccgt gccatcagtg ggctccggtc cgaggatgag gctgattatt 660
actgtgcagc atgggatgac agcctgggat tcggcggagg gaccaagctc accgtcctag 720
gt

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<210> 5
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 5
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 115 120 125
 Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly
 130 135 140
 Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
 145 150 155 160
 Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 165 170 175
 Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro
 180 185 190
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
 195 200 205
 Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
 210 215 220
 Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 225 230 235 240

<210> 6

<211> 729
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Phage Library

<400> 6
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 gagactctcc tgtgcagcct ctggattcac ctttagcagc tatgccatga gctgggtccg 120
 ccaggctcca ggggaagggc tggagtgggt ctgagctatt agtggtagtg gtggtagcac 180
 atactacgca gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac 240
 gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcaag 300
 agctggctgt attttgtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
 tggaggcggg tcaggcggag gtggctctgg cggtagtga cttcagtctg tgctgactca 420
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
 actcctcatc tataggaata atcagcggcc ctgaggggtc cctgaccgat tctctggctc 600
 caagtctggc acctcagcct ccctggccat cagtgggctc cgggccgagg atgaggctga 660
 ttattactgt gcagcatggg atgacagcct ggtattcggc ggagggacca agctgaccgt 720
 cctaggtgc 729

<210> 7
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Phage Library

<400> 7
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 ccggcagccc ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac 180
 caactacaac cctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca 240
 gttctccctg aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcaag 300
 aatgcggaag gataagtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
 tggaggcggg tcaggcggag gtggctctgg cggtagtga cttcagtctg tgctgactca 420
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
 actcctcatc tataggaata atcagcggcc ctgaggggtc cctgaccgat tctctggctc 600
 caagtctggc acctcagcct ccctggccat cagtgggctc cgggccgagg atgaggctga 660
 ttattactgt gcagcatggg atgacagcct gtttgtattc ggcggaggga ccaagctgac 720
 cgtccctaggg gcggccgc 738

<210> 8
 <211> 739
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Phage Library

<400> 8
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 aaggtttccct gcaaggcatc tggatacacc ttcaccagct actatatgca ctgggtgcga 120
 caggccccctg gacaagggct tgagtggatg ggaataatca accctagtgg tggtagcaca 180
 caagctacgc acagaagttc cagggcagag tcaccatgac caggacacg tccacgagca 240
 cagtctacat ggagctgagc agcctgagat ctgaggacac ggccgtgtat tactgtgcaa 300
 gaatggctcc ctatgtgaat acgcttgttt tttggggcca aggtaccctg gtcaccgtct 360
 cgagtgggtg aggcgggtca ggcgagggtg gctctggcgg tagtgactt cagtctgtgc 420
 tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc acatgccaag 480

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly
 130 135 140
 Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
 145 150 155 160
 Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 165 170 175
 Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro
 180 185 190
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
 195 200 205
 Ser Gly Leu Arg Ser Glu Asp Glu Ala Ser Tyr Tyr Cys Ala Ala Trp
 210 215 220
 Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 225 230 235 240

<210> 11
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 11
 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
 1 5 10 15
 Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
 20 25 30
 Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 35 40 45
 Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
 50 55 60
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser
 130 135 140
 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser
 145 150 155 160
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro
 165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser
 180 185 190
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
 195 200 205
 Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val
 210 215 220
 Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu Gly Ala Ala
 245

<210> 12
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 12
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val
 130 135 140
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
 145 150 155 160
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 165 170 175
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
 180 185 190
 Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
 195 200 205
 Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg

210		215		220
Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Gly Thr Lys Leu Thr Val				
225		230		235

Leu Gly

<210> 13
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Phage library

<400> 13
 Gln Val Gln Leu Leu Gln Ser Ala Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 115 120 125
 Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
 130 135 140
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
 145 150 155 160
 Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 165 170 175
 Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser
 180 185 190
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
 195 200 205
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn
 210 215 220
 Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 225 230 235 240

<210> 14

<211> 742
 <212> DNA
 <213> Homo sapiens

<400> 14
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 aagccatggc ttgccttgga tttcagcggc acaaggctca gctgaacctg gctaccagga 120
 cctggccctg cactctcctg ttttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180
 acgtggccca gcctgctgtg gtactggcca gcagccgagg catcgccagc tttgtgtgtg 240
 agtatgcatc tccaggcaaa gccactgagg tccgggtgac agtgcttcgg caggctgaca 300
 gccaggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagttg accttcctag 360
 atgattccat ctgcacgggc acctccagtg gaaatcaagt gaacctcact atccaaggac 420
 tgagggccat ggacacggga ctctacatct gcaagggtgga gctcatgtac ccaccgccat 480
 actacctggg cataggcaac ggaacccaga tttatgtaat tgatccagaa ccgtgcccag 540
 attctgactt cctcctctgg atccttgacag cagttagttc ggggttggtt ttttatagct 600
 ttctcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660
 ggggtctatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720
 ttattcccat caattgagaa tt 742

<210> 15
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
 1 5 10 15
 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
 20 25 30
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
 35 40 45
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
 50 55 60
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
 85 90 95
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125
 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

<210> 16
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 16
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 ctctcgccgc tggccttgct gctccacgcc gccaggccga gccagttccg ggtgtcgccg 120
 ctggatcgga cctggaacct gggcgagaca gtggagctga agtgccaggt gctgctgtcc 180
 aacccgacgt cgggctgctc gtggctcttc cagccgcgcg gcgccgccgc cagtcccacc 240
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 ttctcgggca agaggttggg ggacaccttc gtcctcacc tgagcgactt ccgccgagag 360
 aacgagggct actatttctg ctcgccctg agcaactcca tcatgtactt cagccacttc 420
 gtgccggtct tcctgccagc gaagcccacc acgacgccag cgccgcgacc accaacaccg 480
 gcgcccacca tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg 540
 gggggcgag tgacacagag ggggctggac ttgcctgtg atatctacat ctgggcgccc 600
 ttggccggga cttgtggggt cttctcctg tcactgggta tcacccttta ctgcaaccac 660
 aggaaccgaa gacgtgtttg caaatgtccc cggcctgtgg tcaaatacgg agacaagccc 720
 agcctttcgg cgagatacgt ctaaccctgt gcaacagcca ctacatgaat tcc 773

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 17
 ttgaagctta gccatggctt gctctgga 28

<210> 18
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 18
 taatgaattc tcaattgatg ggaataaaat aag 33

<210> 19
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 19
 cggttctgca gcaccaccgg agccaccatc agaattctggg catggttctg gatcaatgac 60

<210> 20
 <211> 25

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 20
 gagctgaaac gggcggccgc agaac 25
 <210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 21
 ctggcctgca gcattcagat cc 22
 <210> 22
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 22
 ttcaaagctt caggatcctg aaaggttttg 30
 <210> 23
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 23
 taatgaattc tcaattgatg ggaataaaat aag 33
 <210> 24
 <211> 76
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 24
 gatgtagata tcacaggcga agtcgacacc accggagcca ccaattacat aaatctgggc 60
 tccgttgctt atgccc 76
 <210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

 <400> 25
 tcgcgcccaa gcttcgagcc aagcagcgt 29

 <210> 26
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 26
 taatgaattc tcaattgatg ggaataaaat aag 33

 <210> 27
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 27
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 tgatatctac atc 73

 <210> 28
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: linker

 <400> 28
 Gly Gly Ser Gly Gly Ala Ala
 1 5

 <210> 29
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: hexapeptide motif

 <400> 29
 Met Tyr Pro Pro Pro Tyr
 1 5

 <210> 30
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: hexapeptide motif

<400> 30

Leu Tyr Pro Pro Pro Tyr
1 5

<210> 31

<211> 223

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15

Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
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Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
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 Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe
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 Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser
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